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SMITH, KENNETH T.

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Arg Ser Arg Ala His Asn Leu Ser Val Gln Val Lys Lys Gly Pro Trp
20                25                30                35

cag act ttc tgt gcc tct gaa tgg cca aca ttc gat gtt gga tgg cca 740
Gln Thr Phe Cys Ala Ser Glu Trp Pro Thr Phe Asp Val Gly Trp Pro
      40                45                50

tca gag ggg acc ttt aat tct gaa att atc ctg gct gtt aag gca atc 788

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Ser	Glu	Gly	Thr	Phe	Asn	Ser	Glu	Ile	Ile	Leu	Ala	Val	Lys	Ala	Ile		
			55					60					65				
att	ttt	cag	act	gga	ccc	ggc	tct	cat	cct	gat	cag	gag	ccc	tat	atc		836
Ile	Phe	Gln	Thr	Gly	Pro	Gly	Ser	His	Pro	Asp	Gln	Glu	Pro	Tyr	Ile		
		70					75					80					
ctt	acg	tgg	caa	gat	ttg	gca	gaa	gat	cct	ccg	cca	tgg	ggt	aaa	cca		884
Leu	Thr	Trp	Gln	Asp	Leu	Ala	Glu	Asp	Pro	Pro	Pro	Trp	Val	Lys	Pro		
		85				90					95						
tgg	cta	aat	aaa	cca	aga	aag	cca	ggt	ccc	cga	atc	ctg	gct	ctt	gga		932
Trp	Leu	Asn	Lys	Pro	Arg	Lys	Pro	Gly	Pro	Arg	Ile	Leu	Ala	Leu	Gly		
100					105				110						115		
gag	aaa	aac	aaa	cac	tcg	gcc	gaa	aaa	gtc	gag	ccc	tct	tcc	tcg	tat		980
Glu	Lys	Asn	Lys	His	Ser	Ala	Glu	Lys	Val	Glu	Pro	Ser	Ser	Ser	Tyr		
				120					125					130			
cta	ccc	cga	gat	cga	gga	gcc	gcc	gac	ttg	gcc	gga	acc	cca	acc	tgt		1028
Leu	Pro	Arg	Asp	Arg	Gly	Ala	Ala	Asp	Leu	Ala	Gly	Thr	Pro	Thr	Cys		
			135					140					145				
tcc	ccc	acc	ccc	tta	tcc	agc	aca	ggg	tgc	tgt	gag	ggg	acc	tct	gcc		1076
Ser	Pro	Thr	Pro	Leu	Ser	Ser	Thr	Gly	Cys	Cys	Glu	Gly	Thr	Ser	Ala		
		150					155					160					
cct	cct	gga	gct	ccg	gtg	gtg	gag	gga	cct	gct	gcc	ggg	act	cgg	agc		1124
Pro	Pro	Gly	Ala	Pro	Val	Val	Glu	Gly	Pro	Ala	Ala	Gly	Thr	Arg	Ser		
		165				170					175						
cgg	aga	ggc	gcc	acc	ccg	gag	cgg	aca	gac	gag	atc	gcg	ata	tta	ccg		1172
Arg	Arg	Gly	Ala	Thr	Pro	Glu	Arg	Thr	Asp	Glu	Ile	Ala	Ile	Leu	Pro		
180					185				190						195		
ctg	cgc	acc	tat	ggc	cct	ccc	atg	cca	ggg	ggc	caa	ttg	cag	ccc	ctc		1220
Leu	Arg	Thr	Tyr	Gly	Pro	Pro	Met	Pro	Gly	Gly	Gln	Leu	Gln	Pro	Leu		
				200					205					210			
cag	tat	tgg	ccc	ttt	tct	tct	gca	gat	ctc	tat	aat	tgg	aaa	act	aac		1268
Gln	Tyr	Trp	Pro	Phe	Ser	Ser	Ala	Asp	Leu	Tyr	Asn	Trp	Lys	Thr	Asn		
			215					220					225				
cat	ccc	cct	ttc	tcg	gag	gat	ccc	caa	cgc	ctc	acg	ggg	ttg	gtg	gag		1316
His	Pro	Pro	Phe	Ser	Glu	Asp	Pro	Gln	Arg	Leu	Thr	Gly	Leu	Val	Glu		
		230					235					240					
tcc	ctt	atg	ttc	tct	cac	cag	cct	act	tgg	gat	gat	tgt	caa	cag	ctg		1364
Ser	Leu	Met	Phe	Ser	His	Gln	Pro	Thr	Trp	Asp	Asp	Cys	Gln	Gln	Leu		
		245				250					255						
ctg	cag	aca	ctc	ttc	aca	acc	gag	gag	cga	gag	aga	att	ctg	tta	gag		1412
Leu	Gln	Thr	Leu	Phe	Thr	Thr	Glu	Glu	Arg	Glu	Arg	Ile	Leu	Leu	Glu		
		260				265				270					275		
gct	aga	aaa	aat	gtt	cct	ggg	gcc	gac	ggg	cga	ccc	acg	cag	ttg	caa		1460
Ala	Arg	Lys	Asn	Val	Pro	Gly	Ala	Asp	Gly	Arg	Pro	Thr	Gln	Leu	Gln		

280	285	290	
aat gag att gac atg gga ttt ccc ttg act cgc ccc ggt tgg gac tac			1508
Asn Glu Ile Asp Met Gly Phe Pro Leu Thr Arg Pro Gly Trp Asp Tyr			
295	300	305	
aac acg gct gaa ggt agg gag agc ttg aaa atc tat cgc cag gct ctg			1556
Asn Thr Ala Glu Gly Arg Glu Ser Leu Lys Ile Tyr Arg Gln Ala Leu			
310	315	320	
gtg gcg ggt ctc cgg ggc gcc tca aga cgg ccc act aat ttg gct aag			1604
Val Ala Gly Leu Arg Gly Ala Ser Arg Arg Pro Thr Asn Leu Ala Lys			
325	330	335	
gta aga gag gtg atg cag gga ccg aac gaa cct ccc tcg gta ttt ctt			1652
Val Arg Glu Val Met Gln Gly Pro Asn Glu Pro Pro Ser Val Phe Leu			
340	345	350	
gag agg ctc atg gaa gcc ttc agg cgg ttc acc cct ttt gat cct acc			1700
Glu Arg Leu Met Glu Ala Phe Arg Arg Phe Thr Pro Phe Asp Pro Thr			
360	365	370	
tca gag gcc cag aaa gcc tca gtg gcc ctg gcc ttc att ggg cag tcg			1748
Ser Glu Ala Gln Lys Ala Ser Val Ala Leu Ala Phe Ile Gly Gln Ser			
375	380	385	
gct ctg gat atc agg aag aaa ctt cag aga ctg gaa ggg tta cag gag			1796
Ala Leu Asp Ile Arg Lys Lys Leu Gln Arg Leu Glu Gly Leu Gln Glu			
390	395	400	
gct gag tta cgt gat cta gtg aga gag gca gag aag gtg tat tac aga			1844
Ala Glu Leu Arg Asp Leu Val Arg Glu Ala Glu Lys Val Tyr Tyr Arg			
405	410	415	
agg gag aca gaa gag gag aag gaa cag aga aaa gaa aag gag aga gaa			1892
Arg Glu Thr Glu Glu Glu Lys Glu Gln Arg Lys Glu Lys Glu Arg Glu			
420	425	430	
gaa agg gag gaa aga cgt gat aga cgg caa gag aag aat ttg act aag			1940
Glu Arg Glu Glu Arg Arg Asp Arg Arg Gln Glu Lys Asn Leu Thr Lys			
440	445	450	
atc ttg gcc gca gtg gtt gaa ggg aag agc agc agg gag aga gag aga			1988
Ile Leu Ala Ala Val Val Glu Gly Lys Ser Ser Arg Glu Arg Glu Arg			
455	460	465	
gat ttt agg aaa att agg tca ggc cct aga cag tca ggg aac ctg ggc			2036
Asp Phe Arg Lys Ile Arg Ser Gly Pro Arg Gln Ser Gly Asn Leu Gly			
470	475	480	
aat agg acc cca ctc gac aag gac cag tgt gcg tat tgt aaa gaa aaa			2084
Asn Arg Thr Pro Leu Asp Lys Asp Gln Cys Ala Tyr Cys Lys Glu Lys			
485	490	495	
gga cac tgg gca agg aac tgc ccc aag aag gga aac aaa gga ccg aag			2132
Gly His Trp Ala Arg Asn Cys Pro Lys Lys Gly Asn Lys Gly Pro Lys			
500	505	510	

gtc cta gct cta gaa gaa gat aaa gat tag ggg aga cgg ggt tgc gac Val Leu Ala Leu Glu Glu Asp Lys Asp Gly Arg Arg Gly Ser Asp 520 525 530	2180
ccc ctc ccc gag ccc agg gta act ttg aag gtg gag ggg caa cca gtt Pro Leu Pro Glu Pro Arg Val Thr Leu Lys Val Glu Gly Gln Pro Val 535 540 545	2228
gag ttc ctg gtt gat acc gga gcg gag cat tca gtg ctg cta caa cca Glu Phe Leu Val Asp Thr Gly Ala Glu His Ser Val Leu Leu Gln Pro 550 555 560	2276
tta gga aaa cta aaa gaa aaa aaa tcc tgg gtg atg ggt gcc aca ggg Leu Gly Lys Leu Lys Glu Lys Lys Ser Trp Val Met Gly Ala Thr Gly 565 570 575	2324
caa cgg cag tat cca tgg act acc cga aga acc gtt gac ttg gga gtg Gln Arg Gln Tyr Pro Trp Thr Thr Arg Arg Thr Val Asp Leu Gly Val 580 585 590	2372
gga cgg gta acc cac tgc ttt ctg gtc atc cct gag tgc cca gta ccc Gly Arg Val Thr His Ser Phe Leu Val Ile Pro Glu Cys Pro Val Pro 595 600 605 610	2420
ctt cta ggt aga gac tta ctg acc aag atg gga gct caa att tct ttt Leu Leu Gly Arg Asp Leu Leu Thr Lys Met Gly Ala Gln Ile Ser Phe 615 620 625	2468
gaa caa gga aga cca gaa gtg tct gtg aat aac aaa ccc atc act gtg Glu Gln Gly Arg Pro Glu Val Ser Val Asn Asn Lys Pro Ile Thr Val 630 635 640	2516
ttg acc ctc caa tta gat gat gaa tat cga cta tat tct ccc caa gta Leu Thr Leu Gln Leu Asp Asp Glu Tyr Arg Leu Tyr Ser Pro Gln Val 645 650 655	2564
aag cct gat caa gat ata cag tcc tgg ttg gag cag ttt ccc caa gcc Lys Pro Asp Gln Asp Ile Gln Ser Trp Leu Glu Gln Phe Pro Gln Ala 660 665 670	2612
tgg gca gaa acc gca ggg atg ggt ttg gca aag caa gtt ccc cca cag Trp Ala Glu Thr Ala Gly Met Gly Leu Ala Lys Gln Val Pro Pro Gln 675 680 685 690	2660
gtt att caa ctg aag gcc agt gct aca cca gta tca gtc aga cag tac Val Ile Gln Leu Lys Ala Ser Ala Thr Pro Val Ser Val Arg Gln Tyr 695 700 705	2708
ccc ttg agt aga gag gct cga gaa gga att tgg ccg cat gtt caa aga Pro Leu Ser Arg Glu Ala Arg Glu Gly Ile Trp Pro His Val Gln Arg 710 715 720	2756
tta atc caa cag ggc atc cta gtt cct gtc caa tcc cct tgg aat act Leu Ile Gln Gln Gly Ile Leu Val Pro Val Gln Ser Pro Trp Asn Thr 725 730 735	2804

ccc ctg cta ccg gtt agg aag cct ggg acc aat gat tat cga cca gta Pro Leu Leu Pro Val Arg Lys Pro Gly Thr Asn Asp Tyr Arg Pro Val 740 745 750	2852
cag gac ttg aga gag gtc aat aaa agg gtg cag gac ata cac cca acg Gln Asp Leu Arg Glu Val Asn Lys Arg Val Gln Asp Ile His Pro Thr 755 760 765 770	2900
gtc ccg aac cct tat aac ctc ttg agc gcc ctc ccg cct gaa cgg aac Val Pro Asn Pro Tyr Asn Leu Leu Ser Ala Leu Pro Pro Glu Arg Asn 775 780 785	2948
tgg tac aca gta ttg gac tta aaa gat gcc ttc ttc tgc ctg aga tta Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg Leu 790 795 800	2996
cac ccc act agc caa cca ctt ttt gcc ttc gaa tgg aga gat cca ggt His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro Gly 805 810 815	3044
acg gga aga acc ggg cag ctc acc tgg acc cga ctg ccc caa ggg ttc Thr Gly Arg Thr Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly Phe 820 825 830	3092
aag aac tcc ccg acc atc ttt gac gaa gcc cta cac agg gac ctg gcc Lys Asn Ser Pro Thr Ile Phe Asp Glu Ala Leu His Arg Asp Leu Ala 835 840 845 850	3140
aac ttc agg atc caa cac cct cag gtg acc ctc ctc cag tac gtg gat Asn Phe Arg Ile Gln His Pro Gln Val Thr Leu Leu Gln Tyr Val Asp 855 860 865	3188
gac ctg ctt ctg gcg gga gcc acc aaa cag gac tgc tta gaa ggt acg Asp Leu Leu Leu Ala Gly Ala Thr Lys Gln Asp Cys Leu Glu Gly Thr 870 875 880	3236
aag gca cta ctg ctg gaa ttg tct gac cta ggc tac aga gcc tct gct Lys Ala Leu Leu Leu Glu Leu Ser Asp Leu Gly Tyr Arg Ala Ser Ala 885 890 895	3284
aag aag gcc cag att tgc agg aga gag gta aca tac ttg ggg tac agt Lys Lys Ala Gln Ile Cys Arg Arg Glu Val Thr Tyr Leu Gly Tyr Ser 900 905 910	3332
ttg cgg ggc ggg cag cga tgg ctg acg gag gca cgg aag aaa act gta Leu Arg Gly Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Lys Thr Val 915 920 925 930	3380
gtc cag ata ccg gcc cca acc aca gcc aaa caa gtg aga gag ttt ttg Val Gln Ile Pro Ala Pro Thr Thr Ala Lys Gln Val Arg Glu Phe Leu 935 940 945	3428
ggg aca gct gga ttt tgc aga ctg tgg atc ccg ggg ttt gcg acc tta Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Thr Leu 950 955 960	3476
gca gcc cca ctc tac ccg cta acc aaa gaa aaa ggg gga ttc tcc tgg	3524

Ala Ala Pro Leu Tyr Pro Leu Thr Lys Glu Lys Gly Gly Phe Ser Trp	
965	970 975
gct cct gag cac cag aag gca ttt gat gct atc aaa aag gcc ctg ctg	3572
Ala Pro Glu His Gln Lys Ala Phe Asp Ala Ile Lys Lys Ala Leu Leu	
980 985 990	
agc gca cct gct ctg gcc ctc cct gac gta act aaa ccc ttt acc	3617
Ser Ala Pro Ala Leu Ala Leu Pro Asp Val Thr Lys Pro Phe Thr	
995 1000 1005	
ctt tat gtg gat gag cgt aag gga gta gcc cga gga gtt tta acc	3662
Leu Tyr Val Asp Glu Arg Lys Gly Val Ala Arg Gly Val Leu Thr	
1010 1015 1020	
caa acc cta gga cca tgg agg aga cct gtt gcc tac ctg tca aag	3707
Gln Thr Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys	
1025 1030 1035	
aag ctt gat cct gta gcc agt ggt tgg ccc gta tgt ctg aag gct	3752
Lys Leu Asp Pro Val Ala Ser Gly Trp Pro Val Cys Leu Lys Ala	
1040 1045 1050	
atc gca gct gtg gcc ata ctg gtc aag gac gct gac aaa ttg act	3797
Ile Ala Ala Val Ala Ile Leu Val Lys Asp Ala Asp Lys Leu Thr	
1055 1060 1065	
ttg gga cag aat ata act gta ata gcc ccc cat gca ttg gag aac	3842
Leu Gly Gln Asn Ile Thr Val Ile Ala Pro His Ala Leu Glu Asn	
1070 1075 1080	
atc gtt cgg cag ccc cca gac cga tgg atg acc aac gcc cgc atg	3887
Ile Val Arg Gln Pro Pro Asp Arg Trp Met Thr Asn Ala Arg Met	
1085 1090 1095	
acc cac tat caa agc ctg ctt ctc aca gag agg gtc act ttc gct	3932
Thr His Tyr Gln Ser Leu Leu Leu Thr Glu Arg Val Thr Phe Ala	
1100 1105 1110	
cca cca gcc gct ctc aac cct gcc act ctt ctg cct gaa gag act	3977
Pro Pro Ala Ala Leu Asn Pro Ala Thr Leu Leu Pro Glu Glu Thr	
1115 1120 1125	
gat gaa cca gtg act cat gat tgc cat caa cta ttg att gag gag	4022
Asp Glu Pro Val Thr His Asp Cys His Gln Leu Leu Ile Glu Glu	
1130 1135 1140	
act ggg gtc cgc aag gac ctt aca gac ata ccg ctg act gga gaa	4067
Thr Gly Val Arg Lys Asp Leu Thr Asp Ile Pro Leu Thr Gly Glu	
1145 1150 1155	
gtg cta acc tgg ttc act gac gga agc agc tat gtg gtg gaa ggt	4112
Val Leu Thr Trp Phe Thr Asp Gly Ser Ser Tyr Val Val Glu Gly	
1160 1165 1170	
aag agg atg gct ggg gcg gca gtg gtg gac ggg acc cgc acg atc	4157
Lys Arg Met Ala Gly Ala Ala Val Val Asp Gly Thr Arg Thr Ile	

1175	1180	1185	
tgg gcc agc agc ctg ccg gaa gga act tca gcg caa aag gct gag			4202
Trp Ala Ser Ser Leu Pro Glu Gly Thr Ser Ala Gln Lys Ala Glu			
1190	1195	1200	
ctc atg gcc ctc acg caa gct ttg cgg ctg gcc gaa ggg aaa tcc			4247
Leu Met Ala Leu Thr Gln Ala Leu Arg Leu Ala Glu Gly Lys Ser			
1205	1210	1215	
ata aac att tat acg gac agc agg tat gcc ttt gcg act gca cac			4292
Ile Asn Ile Tyr Thr Asp Ser Arg Tyr Ala Phe Ala Thr Ala His			
1220	1225	1230	
gta cac ggg gcc atc tat aaa caa agg ggg ttg ctt acc tca gca			4337
Val His Gly Ala Ile Tyr Lys Gln Arg Gly Leu Leu Thr Ser Ala			
1235	1240	1245	
ggg agg gaa ata aag aac aaa gag gaa att cta agc cta tta gaa			4382
Gly Arg Glu Ile Lys Asn Lys Glu Glu Ile Leu Ser Leu Leu Glu			
1250	1255	1260	
gcc tta cat ttg cca aaa agg cta gct att ata cac tgt cct gga			4427
Ala Leu His Leu Pro Lys Arg Leu Ala Ile Ile His Cys Pro Gly			
1265	1270	1275	
cat cag aaa gcc aaa gat ctc ata tct aga ggg aac cag atg gct			4472
His Gln Lys Ala Lys Asp Leu Ile Ser Arg Gly Asn Gln Met Ala			
1280	1285	1290	
gac cgg gtt gcc aag cag gca gcc cag gct gtt aac ctt ctg cct			4517
Asp Arg Val Ala Lys Gln Ala Ala Gln Ala Val Asn Leu Leu Pro			
1295	1300	1305	
ata ata gaa acg ccc aaa gcc cca gaa ccc aga cga cag tac acc			4562
Ile Ile Glu Thr Pro Lys Ala Pro Glu Pro Arg Arg Gln Tyr Thr			
1310	1315	1320	
cta gaa gac tgg caa gag ata aaa aag ata gac cag ttc tct gag			4607
Leu Glu Asp Trp Gln Glu Ile Lys Lys Ile Asp Gln Phe Ser Glu			
1325	1330	1335	
act ccg gag ggg acc tgc tat acc tca tat ggg aag gaa atc ctg			4652
Thr Pro Glu Gly Thr Cys Tyr Thr Ser Tyr Gly Lys Glu Ile Leu			
1340	1345	1350	
ccc cac aaa gaa ggg tta gaa tat gtc caa cag ata cat cgt cta			4697
Pro His Lys Glu Gly Leu Glu Tyr Val Gln Gln Ile His Arg Leu			
1355	1360	1365	
acc cac cta gga act aaa cac ctg cag cag ttg gtc aga aca tcc			4742
Thr His Leu Gly Thr Lys His Leu Gln Gln Leu Val Arg Thr Ser			
1370	1375	1380	
cct tat cat gtt ctg agg cta cca gga gtg gct gac tcg gtg gtc			4787
Pro Tyr His Val Leu Arg Leu Pro Gly Val Ala Asp Ser Val Val			
1385	1390	1395	

aaa	cat	tgt	gtg	ccc	tgc	cag	ctg	gtt	aat	gct	aat	cct	tcc	aga	4832
Lys	His	Cys	Val	Pro	Cys	Gln	Leu	Val	Asn	Ala	Asn	Pro	Ser	Arg	
1400					1405					1410					
ata	cct	cca	gga	aag	aga	cta	agg	gga	agc	cac	cca	ggc	gct	cac	4877
Ile	Pro	Pro	Gly	Lys	Arg	Leu	Arg	Gly	Ser	His	Pro	Gly	Ala	His	
1415					1420					1425					
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Trp	Glu	Val	Asp	Phe	Thr	Glu	Val	Lys	Pro	Ala	Lys	Tyr	Gly	Asn	
1430					1435					1440					
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Lys	Tyr	Leu	Leu	Val	Phe	Val	Asp	Thr	Phe	Ser	Gly	Trp	Val	Glu	
1445					1450					1455					
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Ala	Tyr	Pro	Thr	Lys	Lys	Glu	Thr	Ser	Thr	Val	Val	Ala	Lys	Lys	
1460					1465					1470					
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Ile	Leu	Glu	Glu	Ile	Phe	Pro	Arg	Phe	Gly	Ile	Pro	Lys	Val	Ile	
1475					1480					1485					
ggg	tca	gac	aat	ggg	cca	gct	ttc	gtt	gcc	cag	gta	agt	cag	gga	5102
Gly	Ser	Asp	Asn	Gly	Pro	Ala	Phe	Val	Ala	Gln	Val	Ser	Gln	Gly	
1490					1495					1500					
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Leu	Ala	Lys	Ile	Leu	Gly	Ile	Asp	Trp	Lys	Leu	His	Cys	Ala	Tyr	
1505					1510					1515					
aga	ccc	caa	agc	tca	gga	cag	gta	gag	agg	atg	aat	aga	acc	att	5192
Arg	Pro	Gln	Ser	Ser	Gly	Gln	Val	Glu	Arg	Met	Asn	Arg	Thr	Ile	
1520					1525					1530					
aaa	gag	acc	ctt	acc	aaa	ttg	acc	aca	gag	act	ggc	att	aat	gat	5237
Lys	Glu	Thr	Leu	Thr	Lys	Leu	Thr	Thr	Glu	Thr	Gly	Ile	Asn	Asp	
1535					1540					1545					
tgg	atg	gct	ctc	ctg	ccc	ttt	gtg	ctt	ttt	agg	gtg	agg	aac	acc	5282
Trp	Met	Ala	Leu	Leu	Pro	Phe	Val	Leu	Phe	Arg	Val	Arg	Asn	Thr	
1550					1555					1560					
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Pro	Gly	Gln	Phe	Gly	Leu	Thr	Pro	Tyr	Glu	Leu	Leu	Tyr	Gly	Gly	
1565					1570					1575					
ccc	ccc	ccg	ttg	gca	gaa	att	gcc	ttt	gca	cat	agt	gct	gat	gtg	5372
Pro	Pro	Pro	Leu	Ala	Glu	Ile	Ala	Phe	Ala	His	Ser	Ala	Asp	Val	
1580					1585					1590					
ctg	ctt	tcc	cag	cct	ttg	ttc	tct	agg	ctc	aag	gcg	ctc	gag	tgg	5417
Leu	Leu	Ser	Gln	Pro	Leu	Phe	Ser	Arg	Leu	Lys	Ala	Leu	Glu	Trp	
1595					1600					1605					

[illegible]

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acagttgggc	cttgcttaat	taatagggtt	gttgcccttg	ttagagaacg	agtgagtgca	7524
gtccagatca	tggtacttag	gcaacagtac	caaggccttc	tgagccaagg	agaaactgac	7584
ctctagcctt	cccagttcta	agattagaac	tattaacaag	acaagaagtg	gggaatgaaa	7644
ggatgaaaat	gcaacctaac	cctcccagaa	cccaggaagt	taataaaaag	ctctaaatgc	7704
ccccgaatta	cagaccctgc	tggctgccag	taaataggta	gaaggtcaca	cttcctattg	7764
ttccagggcc	tgctatcctg	gcctaagtaa	gataacagga	aatgagttga	ctaactgctt	7824
atctggattc	tgtaaaactg	actggcacca	tagaagaatt	gattacacat	tgacagccct	7884
agtgaacctat	ctcaactgca	atctgtcact	ctgcccagga	gcccacgcag	atgcggacct	7944
ccggagctat	tttaaaatga	ttggtccacg	gagcgcgggc	tctcgatatt	ttaaaatgat	8004
tggtccatgg	agcgcgggct	ctcgatattt	taaaatgatt	ggtttgtgac	gcacaggctt	8064
tgttgtgaac	cccataaaaag	ctgtcccgat	tccgcactcg	gggccgcagt	cctctacccc	8124
tgctgtgtgt	acgactgtgg	gccccagcgc	gcttgaata	aaaatcctct	tgctgtttgc	8184
atcaaaaaaa	aaaaaaaaaa	aaaaa				8209

<210> 4
 <211> 524
 <212> PRT
 <213> Porcine retrovirus

<400> 4
 Met Gly Gln Thr Val Thr Thr Pro Leu Ser Leu Thr Leu Asp His Trp
 1 5 10 15
 Thr Glu Val Arg Ser Arg Ala His Asn Leu Ser Val Gln Val Lys Lys
 20 25 30
 Gly Pro Trp Gln Thr Phe Cys Ala Ser Glu Trp Pro Thr Phe Asp Val
 35 40 45
 Gly Trp Pro Ser Glu Gly Thr Phe Asn Ser Glu Ile Ile Leu Ala Val
 50 55 60
 Lys Ala Ile Ile Phe Gln Thr Gly Pro Gly Ser His Pro Asp Gln Glu
 65 70 75 80
 Pro Tyr Ile Leu Thr Trp Gln Asp Leu Ala Glu Asp Pro Pro Pro Trp
 85 90 95
 Val Lys Pro Trp Leu Asn Lys Pro Arg Lys Pro Gly Pro Arg Ile Leu
 100 105 110
 Ala Leu Gly Glu Lys Asn Lys His Ser Ala Glu Lys Val Glu Pro Ser
 115 120 125
 Ser Ser Tyr Leu Pro Arg Asp Arg Gly Ala Ala Asp Leu Ala Gly Thr
 130 135 140
 Pro Thr Cys Ser Pro Thr Pro Leu Ser Ser Thr Gly Cys Cys Glu Gly
 145 150 155 160
 Thr Ser Ala Pro Pro Gly Ala Pro Val Val Glu Gly Pro Ala Ala Gly
 165 170 175
 Thr Arg Ser Arg Arg Gly Ala Thr Pro Glu Arg Thr Asp Glu Ile Ala
 180 185 190
 Ile Leu Pro Leu Arg Thr Tyr Gly Pro Pro Met Pro Gly Gly Gln Leu
 195 200 205
 Gln Pro Leu Gln Tyr Trp Pro Phe Ser Ser Ala Asp Leu Tyr Asn Trp
 210 215 220
 Lys Thr Asn His Pro Pro Phe Ser Glu Asp Pro Gln Arg Leu Thr Gly
 225 230 235 240
 Leu Val Glu Ser Leu Met Phe Ser His Gln Pro Thr Trp Asp Asp Cys
 245 250 255
 Gln Gln Leu Leu Gln Thr Leu Phe Thr Thr Glu Glu Arg Glu Arg Ile
 260 265 270

Leu Leu Glu Ala Arg Lys Asn Val Pro Gly Ala Asp Gly Arg Pro Thr
 275 280 285
 Gln Leu Gln Asn Glu Ile Asp Met Gly Phe Pro Leu Thr Arg Pro Gly
 290 295 300
 Trp Asp Tyr Asn Thr Ala Glu Gly Arg Glu Ser Leu Lys Ile Tyr Arg
 305 310 315 320
 Gln Ala Leu Val Ala Gly Leu Arg Gly Ala Ser Arg Arg Pro Thr Asn
 325 330 335
 Leu Ala Lys Val Arg Glu Val Met Gln Gly Pro Asn Glu Pro Pro Ser
 340 345 350
 Val Phe Leu Glu Arg Leu Met Glu Ala Phe Arg Arg Phe Thr Pro Phe
 355 360 365
 Asp Pro Thr Ser Glu Ala Gln Lys Ala Ser Val Ala Leu Ala Phe Ile
 370 375 380
 Gly Gln Ser Ala Leu Asp Ile Arg Lys Lys Leu Gln Arg Leu Glu Gly
 385 390 395 400
 Leu Gln Glu Ala Glu Leu Arg Asp Leu Val Arg Glu Ala Glu Lys Val
 405 410 415
 Tyr Tyr Arg Arg Glu Thr Glu Glu Glu Lys Glu Gln Arg Lys Glu Lys
 420 425 430
 Glu Arg Glu Glu Arg Glu Glu Arg Arg Asp Arg Arg Gln Glu Lys Asn
 435 440 445
 Leu Thr Lys Ile Leu Ala Ala Val Val Glu Gly Lys Ser Ser Arg Glu
 450 455 460
 Arg Glu Arg Asp Phe Arg Lys Ile Arg Ser Gly Pro Arg Gln Ser Gly
 465 470 475 480
 Asn Leu Gly Asn Arg Thr Pro Leu Asp Lys Asp Gln Cys Ala Tyr Cys
 485 490 495
 Lys Glu Lys Gly His Trp Ala Arg Asn Cys Pro Lys Lys Gly Asn Lys
 500 505 510
 Gly Pro Lys Val Leu Ala Leu Glu Glu Asp Lys Asp
 515 520

<210> 5

<211> 1194

<212> PRT

<213> Porcine retrovirus

<400> 5

Gly Arg Arg Gly Ser Asp Pro Leu Pro Glu Pro Arg Val Thr Leu Lys

1	5	10	15
Val Glu Gly Gln Pro Val Glu Phe Leu Val Asp Thr Gly Ala Glu His	20	25	30
Ser Val Leu Leu Gln Pro Leu Gly Lys Leu Lys Glu Lys Lys Ser Trp	35	40	45
Val Met Gly Ala Thr Gly Gln Arg Gln Tyr Pro Trp Thr Thr Arg Arg	50	55	60
Thr Val Asp Leu Gly Val Gly Arg Val Thr His Ser Phe Leu Val Ile	65	70	75
Pro Glu Cys Pro Val Pro Leu Leu Gly Arg Asp Leu Leu Thr Lys Met	85	90	95
Gly Ala Gln Ile Ser Phe Glu Gln Gly Arg Pro Glu Val Ser Val Asn	100	105	110
Asn Lys Pro Ile Thr Val Leu Thr Leu Gln Leu Asp Asp Glu Tyr Arg	115	120	125
Leu Tyr Ser Pro Gln Val Lys Pro Asp Gln Asp Ile Gln Ser Trp Leu	130	135	140
Glu Gln Phe Pro Gln Ala Trp Ala Glu Thr Ala Gly Met Gly Leu Ala	145	150	155
Lys Gln Val Pro Pro Gln Val Ile Gln Leu Lys Ala Ser Ala Thr Pro	165	170	175
Val Ser Val Arg Gln Tyr Pro Leu Ser Arg Glu Ala Arg Glu Gly Ile	180	185	190
Trp Pro His Val Gln Arg Leu Ile Gln Gln Gly Ile Leu Val Pro Val	195	200	205
Gln Ser Pro Trp Asn Thr Pro Leu Leu Pro Val Arg Lys Pro Gly Thr	210	215	220
Asn Asp Tyr Arg Pro Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val	225	230	235
Gln Asp Ile His Pro Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Ala	245	250	255
Leu Pro Pro Glu Arg Asn Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala	260	265	270
Phe Phe Cys Leu Arg Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe	275	280	285
Glu Trp Arg Asp Pro Gly Thr Gly Arg Thr Gly Gln Leu Thr Trp Thr	290	295	300
Arg Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Ile Phe Asp Glu Ala			

305	310	315	320
Leu His Arg Asp	Leu Ala Asn Phe Arg	Ile Gln His Pro Gln Val Thr	
325		330	335
Leu Leu Gln Tyr Val Asp Asp	Leu Leu Leu Ala Gly Ala Thr Lys Gln		
340	345	350	
Asp Cys Leu Glu Gly Thr Lys	Ala Leu Leu Leu Glu Leu Ser Asp Leu		
355	360	365	
Gly Tyr Arg Ala Ser Ala Lys Lys Ala Gln Ile Cys Arg Arg Glu Val			
370	375	380	
Thr Tyr Leu Gly Tyr Ser Leu Arg Gly Gly Gln Arg Trp Leu Thr Glu			
385	390	395	400
Ala Arg Lys Lys Thr Val Val Gln Ile Pro Ala Pro Thr Thr Ala Lys			
405	410		415
Gln Val Arg Glu Phe Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile			
420	425		430
Pro Gly Phe Ala Thr Leu Ala Ala Pro Leu Tyr Pro Leu Thr Lys Glu			
435	440		445
Lys Gly Gly Phe Ser Trp Ala Pro Glu His Gln Lys Ala Phe Asp Ala			
450	455	460	
Ile Lys Lys Ala Leu Leu Ser Ala Pro Ala Leu Ala Leu Pro Asp Val			
465	470	475	480
Thr Lys Pro Phe Thr Leu Tyr Val Asp Glu Arg Lys Gly Val Ala Arg			
485	490		495
Gly Val Leu Thr Gln Thr Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr			
500	505		510
Leu Ser Lys Lys Leu Asp Pro Val Ala Ser Gly Trp Pro Val Cys Leu			
515	520		525
Lys Ala Ile Ala Ala Val Ala Ile Leu Val Lys Asp Ala Asp Lys Leu			
530	535	540	
Thr Leu Gly Gln Asn Ile Thr Val Ile Ala Pro His Ala Leu Glu Asn			
545	550	555	560
Ile Val Arg Gln Pro Pro Asp Arg Trp Met Thr Asn Ala Arg Met Thr			
565	570		575
His Tyr Gln Ser Leu Leu Leu Thr Glu Arg Val Thr Phe Ala Pro Pro			
580	585		590
Ala Ala Leu Asn Pro Ala Thr Leu Leu Pro Glu Glu Thr Asp Glu Pro			
595	600		605
Val Thr His Asp Cys His Gln Leu Leu Ile Glu Glu Thr Gly Val Arg			

610	615	620
Lys Asp Leu Thr Asp Ile Pro Leu Thr Gly Glu Val Leu Thr Trp Phe 625	630	635 640
Thr Asp Gly Ser Ser Tyr Val Val Glu Gly Lys Arg Met Ala Gly Ala 645	650	655
Ala Val Val Asp Gly Thr Arg Thr Ile Trp Ala Ser Ser Leu Pro Glu 660	665	670
Gly Thr Ser Ala Gln Lys Ala Glu Leu Met Ala Leu Thr Gln Ala Leu 675	680	685
Arg Leu Ala Glu Gly Lys Ser Ile Asn Ile Tyr Thr Asp Ser Arg Tyr 690	695	700
Ala Phe Ala Thr Ala His Val His Gly Ala Ile Tyr Lys Gln Arg Gly 705	710	715 720
Leu Leu Thr Ser Ala Gly Arg Glu Ile Lys Asn Lys Glu Glu Ile Leu 725	730	735
Ser Leu Leu Glu Ala Leu His Leu Pro Lys Arg Leu Ala Ile Ile His 740	745	750
Cys Pro Gly His Gln Lys Ala Lys Asp Leu Ile Ser Arg Gly Asn Gln 755	760	765
Met Ala Asp Arg Val Ala Lys Gln Ala Ala Gln Ala Val Asn Leu Leu 770	775	780
Pro Ile Ile Glu Thr Pro Lys Ala Pro Glu Pro Arg Arg Gln Tyr Thr 785	790	795 800
Leu Glu Asp Trp Gln Glu Ile Lys Lys Ile Asp Gln Phe Ser Glu Thr 805	810	815
Pro Glu Gly Thr Cys Tyr Thr Ser Tyr Gly Lys Glu Ile Leu Pro His 820	825	830
Lys Glu Gly Leu Glu Tyr Val Gln Gln Ile His Arg Leu Thr His Leu 835	840	845
Gly Thr Lys His Leu Gln Gln Leu Val Arg Thr Ser Pro Tyr His Val 850	855	860
Leu Arg Leu Pro Gly Val Ala Asp Ser Val Val Lys His Cys Val Pro 865	870	875 880
Cys Gln Leu Val Asn Ala Asn Pro Ser Arg Ile Pro Pro Gly Lys Arg 885	890	895
Leu Arg Gly Ser His Pro Gly Ala His Trp Glu Val Asp Phe Thr Glu 900	905	910
Val Lys Pro Ala Lys Tyr Gly Asn Lys Tyr Leu Leu Val Phe Val Asp		

915	920	925
Thr Phe Ser Gly Trp Val Glu Ala Tyr Pro Thr Lys Lys Glu Thr Ser		
930	935	940
Thr Val Val Ala Lys Lys Ile Leu Glu Glu Ile Phe Pro Arg Phe Gly		
945	950	955 960
Ile Pro Lys Val Ile Gly Ser Asp Asn Gly Pro Ala Phe Val Ala Gln		
	965	970 975
Val Ser Gln Gly Leu Ala Lys Ile Leu Gly Ile Asp Trp Lys Leu His		
	980	985 990
Cys Ala Tyr Arg Pro Gln Ser Ser Gly Gln Val Glu Arg Met Asn Arg		
	995	1000 1005
Thr Ile Lys Glu Thr Leu Thr Lys Leu Thr Thr Glu Thr Gly Ile Asn		
	1010	1015 1020
Asp Trp Met Ala Leu Leu Pro Phe Val Leu Phe Arg Val Arg Asn Thr		
	1025	1030 1035 1040
Pro Gly Gln Phe Gly Leu Thr Pro Tyr Glu Leu Leu Tyr Gly Gly Pro		
	1045	1050 1055
Pro Pro Leu Ala Glu Ile Ala Phe Ala His Ser Ala Asp Val Leu Leu		
	1060	1065 1070
Ser Gln Pro Leu Phe Ser Arg Leu Lys Ala Leu Glu Trp Val Arg Gln		
	1075	1080 1085
Arg Ala Trp Lys Gln Leu Arg Glu Ala Tyr Ser Gly Gly Asp Leu Gln		
	1090	1095 1100
Val Pro His Arg Phe Gln Val Gly Asp Ser Val Tyr Val Arg Arg His		
	1105	1110 1115 1120
Arg Ala Gly Asn Leu Glu Thr Arg Trp Lys Gly Pro Tyr Leu Val Leu		
	1125	1130 1135
Leu Thr Thr Pro Thr Ala Val Lys Val Glu Gly Ile Pro Thr Trp Ile		
	1140	1145 1150
His Ala Ser His Val Lys Pro Ala Pro Pro Pro Asp Ser Gly Trp Arg		
	1155	1160 1165
Ala Glu Lys Thr Glu Asn Pro Leu Lys Leu Arg Leu His Arg Leu Val		
	1170	1175 1180
Pro Tyr Ser Asn Asn Asn Ser Pro Gly Gln		
	1185	1190

<210> 6

<211> 656

<212> PRT

<213> Porcine retrovirus

<400> 6

Met His Pro Thr Leu Ser Arg Arg His Leu Pro Thr Arg Gly Gly Glu
 1 5 10 15
 Pro Lys Arg Leu Arg Ile Pro Leu Ser Phe Ala Ser Ile Ala Trp Phe
 20 25 30
 Leu Thr Leu Thr Ile Thr Pro Gln Ala Ser Ser Lys Arg Leu Ile Asp
 35 40 45
 Ser Ser Asn Pro His Arg Pro Leu Ser Leu Thr Trp Leu Ile Ile Asp
 50 55 60
 Pro Asp Thr Gly Val Thr Val Asn Ser Thr Arg Gly Val Ala Pro Arg
 65 70 75 80
 Gly Thr Trp Trp Pro Glu Leu His Phe Cys Leu Arg Leu Ile Asn Pro
 85 90 95
 Ala Val Lys Ser Thr Pro Pro Asn Leu Val Arg Ser Tyr Gly Phe Tyr
 100 105 110
 Cys Cys Pro Gly Thr Glu Lys Glu Lys Tyr Cys Gly Gly Ser Gly Glu
 115 120 125
 Ser Phe Cys Arg Arg Trp Ser Cys Val Thr Ser Asn Asp Gly Asp Trp
 130 135 140
 Lys Trp Pro Ile Ser Leu Gln Asp Arg Val Lys Phe Ser Phe Val Asn
 145 150 155 160
 Ser Gly Pro Gly Lys Tyr Lys Met Met Lys Leu Tyr Lys Asp Lys Ser
 165 170 175
 Cys Ser Pro Ser Asp Leu Asp Tyr Leu Lys Ile Ser Phe Thr Glu Arg
 180 185 190
 Lys Thr Gly Lys Tyr Ser Lys Val Asp Lys Trp Tyr Glu Leu Gly Asn
 195 200 205
 Ser Phe Leu Leu Tyr Gly Gly Gly Ala Gly Ser Thr Leu Thr Ile Arg
 210 215 220
 Leu Arg Ile Glu Thr Gly Thr Glu Pro Pro Val Ala Met Gly Pro Asp
 225 230 235 240
 Lys Val Leu Ala Glu Gln Gly Pro Pro Ala Leu Glu Pro Pro His Asn
 245 250 255
 Leu Pro Val Pro Gln Leu Thr Ser Leu Arg Pro Asp Ile Thr Gln Pro
 260 265 270
 Pro Ser Asn Ser Thr Thr Gly Leu Ile Pro Thr Asn Thr Pro Arg Asn
 275 280 285

Ser Pro Gly Val Pro Val Lys Thr Gly Gln Arg Leu Phe Ser Leu Ile
 290 295 300
 Gln Gly Ala Phe Gln Ala Ile Asn Ser Thr Asp Pro Asp Ala Thr Ser
 305 310 315 320
 Ser Cys Trp Leu Cys Leu Ser Ser Gly Pro Pro Tyr Tyr Glu Gly Met
 325 330 335
 Ala Lys Glu Arg Lys Phe Asn Val Thr Lys Glu His Arg Asn Gln Cys
 340 345 350
 Thr Trp Gly Ser Arg Asn Lys Leu Thr Leu Thr Glu Val Ser Gly Lys
 355 360 365
 Gly Thr Cys Ile Gly Lys Ala Pro Pro Ser His Gln His Leu Cys Tyr
 370 375 380
 Ser Thr Val Val Tyr Glu Gln Ala Ser Glu Asn Gln Tyr Leu Val Pro
 385 390 395 400
 Gly Tyr Asn Arg Trp Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Val
 405 410 415
 Ser Thr Ser Val Phe Asn Gln Ser Lys Asp Phe Cys Val Met Val Gln
 420 425 430
 Ile Val Pro Arg Val Tyr Tyr His Pro Glu Glu Val Val Leu Asp Glu
 435 440 445
 Tyr Asp Tyr Arg Tyr Asn Arg Pro Lys Arg Glu Pro Val Ser Leu Thr
 450 455 460
 Leu Ala Val Met Leu Gly Leu Gly Thr Ala Val Gly Val Gly Thr Gly
 465 470 475 480
 Thr Ala Ala Leu Ile Thr Gly Pro Gln Gln Leu Glu Lys Gly Leu Gly
 485 490 495
 Glu Leu His Ala Ala Met Thr Glu Asp Leu Arg Ala Leu Lys Glu Ser
 500 505 510
 Val Ser Asn Leu Glu Glu Ser Leu Thr Ser Leu Ser Glu Val Val Leu
 515 520 525
 Gln Asn Arg Arg Gly Leu Asp Leu Leu Phe Leu Arg Glu Gly Gly Leu
 530 535 540
 Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe Tyr Val Asp His Ser Gly
 545 550 555 560
 Ala Ile Arg Asp Ser Met Asn Lys Leu Arg Lys Lys Leu Glu Arg Arg
 565 570 575
 Arg Arg Glu Arg Glu Ala Asp Gln Gly Trp Phe Glu Gly Trp Phe Asn
 580 585 590

Arg Ser Pro Trp Met Thr Thr Leu Leu Ser Ala Leu Thr Gly Pro Leu
595 600 605

Val Val Leu Leu Leu Leu Thr Val Gly Pro Cys Leu Ile Asn Arg
610 615 620

Phe Val Ala Phe Val Arg Glu Arg Val Ser Ala Val Gln Ile Met Val
625 630 635 640

Leu Arg Gln Gln Tyr Gln Gly Leu Leu Ser Gln Gly Glu Thr Asp Leu
645 650 655

<210> 7

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide
designed against Porcine retrovirus genome

<400> 7

ggaagtggac ttcactga

18

<210> 8

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Oligonucleotide
designed against Porcine retrovirus genome

<400> 8

ctttccaccc cgaatcgg

18

<210> 9

<211> 2956

<212> DNA

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Genomic "Raji"
clone DNA ENV region

<400> 9

tgcttttttag ggtaggaac acccctggac agtttgggct gacccctat gaattgctct 60
acgggggacc cccccgttg gtagaaattg cttctgtaca tagtgctgat gtgctgcttt 120
cccagccttt gttctctagg ctcaaggcgc tcgagtgggt gaggcaacga gcgtggaagc 180
agctccggga ggcctactca ggagagagag acttgcaagt tccacatcgc ttccaagttg 240
gagattcagt ctatgttaga cgccaccgtg caggaaacct cgagactcgg tggaagggac 300
cttatctcgt acttttgacc acaccaacgg ctgtgaaagt cgaaggaatc tccacctgga 360
tccatgcata ccacgttaag ctggcgccac ctcccgaact ggggtggaga gccgaaaaga 420
ctgagaatcc ccttaagctt cgcctccatc gcctgggttc ttactctaac aataactccc 480

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caggccagta gtaaacgcct tatagacagc tcgaaccccc atagaccttt atccccctacc 540
tggctgatta ttgacctga tacgggtgtc actgtaaata gcactcgagg tgttgctcct 600
agaggcacct ggtggcctga actgcatttc tgccctccgat tgattaacct cgctgttaaa 660
agcacacctc ccaacctagt ccgtagttat gggttctatt gctgccaggg cacagagaaa 720
gagaaatact gtgggggttc tggggaatcc ttctgtagga gatggagctg cgtcacctcc 780
aacgatggag actggaaatg gccgatctct ctccaggacc gggtaaaatt ctcttttgtc 840
aattccggcc cgggcaagta caaaatgatg aaactatata aagataagag ctgctcccca 900
tcagacttag attatctaaa gataagtttc actgaaaaag gaaaacagga aaatattcaa 960
aagtggataa atgggtatgag ctggggaata gttttttaat aatatggcgg gggagcaggg 1020
tccactttta ccattgcctt taggatagag acggggacag aacccctgt ggcaattggga 1080
cccgataaag tactggctga acaggggccc ccggccctgg agccaccgca taacttgccg 1140
gtgcccgaat taacctcgct gcggcctgac ataacacagc cgcctagcaa cagtaccact 1200
ggattgattc ctaccaacac gcctagaaac tccccagggtg ttctgttaa gacaggacag 1260
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gaaagaaaat tcaatgtgac caaagagcat agaaatcaat gtacatgggg gtcccgaat 1440
aagcttacct tcaactgaag ttccgggaag gggacatgca taggaaaagc tccccatcc 1500
caccaacacc tttgctatag tactgtggtt tatgagcagg cctcagaaaa tcagtattta 1560
gtacctgggt ataacagggt gtgggcatgc aatactgggt taacccctg tgtttccacc 1620
tcagtcttca accaatccaa agatttgtgt gtcatggtcc aaatcgctcc ccgagtgtac 1680
taccatcctg aggaagtggg ccttgatgaa tatgactatc ggtataaccg accaaaaaga 1740
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tccttgactt ctttgtctga agtggttcta cagaaccgga ggggattaga tctgctgttt 1980
ctaagagaag gtgggttatg tgcagcctta aaagaagaat gttgcttcta tgtagatcac 2040
tcaggagcca tcagagactc catgaacaag cttagaaaaa agttagagag gcgtcgaagg 2100
gaaagagagg ctgaccaggg gtggtttgaa ggatggttca acaggtctcc ttggatgacc 2160
accctgcttt ctgctctgac ggggccccta gtagtctgc tcctgttact tacagtggg 2220
ccttgcttaa ttaataggtt tgttgctttt gttagagaac gagtgagtgc agtccagatc 2280
atggtactta ggcaacagta ccaaggcctt ctgagccaag gagaaactga cctctagcct 2340
tcccagttct aagattagaa ctattaacaa gacaagaagt ggggaatgaa aggatgaaaa 2400
tgcaacctaa ccctcccaga acccaggaag ttaataaaaa gctctaaatg cccccgaatt 2460
acagaccctg ctggctgccg gtaaataggt agaaggtcac acttctatt gttccagggc 2520
ctgctatcct ggcctaagta agataacagg aaatgagttg actaatcgct tatctggatt 2580
ctgtaaaact gactggcacc atagaagaat tgattacaca ttgacagccc tagtgacct 2640
tctcaactgc aatctgtcac tctgcccagg agcccacgca gatgcggacc tccggagcta 2700
ttttaaaatg attggtccac ggagcgcggg ctctcgatat tttaaaatga ttggtccatg 2760
gagcgcgggc tctcgatatt ttaaaatgat tggtttgtga cgcacaggct ttgttgtgaa 2820
cccataaaa gctgtcccga ttccgcactc ggggcgcgag tcctctacct ctgctgggtg 2880
tacgactgtg ggccccagcg cgcttggaaat aaaaatctc ttgctgtttg catcaaaaaa 2940
aaaaaaaaa aaaaaa 2956

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<210> 10

<211> 657

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Amino acid sequence
of ENV region "Raji"

<400> 10

Met His Pro Thr Leu Ser Trp Arg His Leu Pro Thr Arg Gly Gly Glu
1 5 10 15

Pro Lys Arg Leu Arg Ile Pro Leu Ser Phe Ala Ser Ile Ala Trp Phe
 20 25 30
 Leu Thr Leu Thr Ile Thr Pro Gln Ala Ser Ser Lys Arg Leu Ile Asp
 35 40 45
 Ser Ser Asn Pro His Arg Pro Leu Ser Pro Thr Trp Leu Ile Ile Asp
 50 55 60
 Pro Asp Thr Gly Val Thr Val Asn Ser Thr Arg Gly Val Ala Pro Arg
 65 70 75 80
 Gly Thr Trp Trp Pro Glu Leu His Phe Cys Leu Arg Leu Ile Asn Pro
 85 90 95
 Ala Val Lys Ser Thr Pro Pro Asn Leu Val Arg Ser Tyr Gly Phe Tyr
 100 105 110
 Cys Cys Pro Gly Thr Glu Lys Glu Lys Tyr Cys Gly Gly Ser Gly Glu
 115 120 125
 Ser Phe Cys Arg Arg Trp Ser Cys Val Thr Ser Asn Asp Gly Asp Trp
 130 135 140
 Lys Trp Pro Ile Ser Leu Gln Asp Arg Val Lys Phe Ser Phe Val Asn
 145 150 155 160
 Ser Gly Pro Gly Lys Tyr Lys Met Met Lys Leu Tyr Lys Asp Lys Ser
 165 170 175
 Cys Ser Pro Ser Asp Leu Asp Tyr Leu Lys Ile Ser Phe Thr Glu Lys
 180 185 190
 Gly Lys Gln Glu Asn Ile Gln Lys Trp Ile Asn Gly Met Ser Trp Gly
 195 200 205
 Ile Val Phe Tyr Lys Tyr Gly Gly Gly Ala Gly Ser Thr Leu Thr Ile
 210 215 220
 Arg Leu Arg Ile Glu Thr Gly Thr Glu Pro Pro Val Ala Met Gly Pro
 225 230 235 240
 Asp Lys Val Leu Ala Glu Gln Gly Pro Pro Ala Leu Glu Pro Pro His
 245 250 255
 Asn Leu Pro Val Pro Gln Leu Thr Ser Leu Arg Pro Asp Ile Thr Gln
 260 265 270
 Pro Pro Ser Asn Ser Thr Thr Gly Leu Ile Pro Thr Asn Thr Pro Arg
 275 280 285
 Asn Ser Pro Gly Val Pro Val Lys Thr Gly Gln Arg Leu Phe Ser Leu
 290 295 300
 Ile Gln Gly Ala Phe Gln Ala Ile Asn Ser Thr Asp Pro Asp Ala Thr
 305 310 315 320

Ser Ser Cys Trp Leu Cys Leu Ser Ser Gly Pro Pro Tyr Tyr Glu Gly
 325 330 335
 Met Ala Lys Glu Arg Lys Phe Asn Val Thr Lys Glu His Arg Asn Gln
 340 345 350
 Cys Thr Trp Gly Ser Arg Asn Lys Leu Thr Leu Thr Glu Val Ser Gly
 355 360 365
 Lys Gly Thr Cys Ile Gly Lys Ala Pro Pro Ser His Gln His Leu Cys
 370 375 380
 Tyr Ser Thr Val Val Tyr Glu Gln Ala Ser Glu Asn Gln Tyr Leu Val
 385 390 395 400
 Pro Gly Tyr Asn Arg Trp Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys
 405 410 415
 Val Ser Thr Ser Val Phe Asn Gln Ser Lys Asp Leu Cys Val Met Val
 420 425 430
 Gln Ile Val Pro Arg Val Tyr Tyr His Pro Glu Glu Val Val Leu Asp
 435 440 445
 Glu Tyr Asp Tyr Arg Tyr Asn Arg Pro Lys Arg Glu Pro Val Ser Leu
 450 455 460
 Thr Leu Ala Val Met Leu Gly Leu Gly Thr Ala Val Gly Val Gly Thr
 465 470 475 480
 Gly Thr Ala Ala Leu Ile Thr Gly Pro Gln Gln Leu Glu Lys Gly Leu
 485 490 495
 Gly Glu Leu His Ala Ala Met Thr Glu Asp Leu Arg Ala Leu Lys Glu
 500 505 510
 Ser Val Ser Asn Leu Glu Glu Ser Leu Thr Ser Leu Ser Glu Val Val
 515 520 525
 Leu Gln Asn Arg Arg Gly Leu Asp Leu Leu Phe Leu Arg Glu Gly Gly
 530 535 540
 Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe Tyr Val Asp His Ser
 545 550 555 560
 Gly Ala Ile Arg Asp Ser Met Asn Lys Leu Arg Lys Lys Leu Glu Arg
 565 570 575
 Arg Arg Arg Glu Arg Glu Ala Asp Gln Gly Trp Phe Glu Gly Trp Phe
 580 585 590
 Asn Arg Ser Pro Trp Met Thr Thr Leu Leu Ser Ala Leu Thr Gly Pro
 595 600 605
 Leu Val Val Leu Leu Leu Leu Leu Thr Val Gly Pro Cys Leu Ile Asn
 610 615 620

Arg Phe Val Ala Phe Val Arg Glu Arg Val Ser Ala Val Gln Ile Met
625 630 635 640

Val Leu Arg Gln Gln Tyr Gln Gly Leu Leu Ser Gln Gly Glu Thr Asp
645 650 655

Leu

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide

<400> 11
gatggctctc ctgccctttg 20

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<213> Porcine retrovirus

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<213> Porcine retrovirus

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<210> 16

<211> 5

<212> PRT

<213> Porcine retrovirus

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Arg Leu Gly Glu Thr

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<210> 17

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<212> DNA

<213> Porcine retrovirus

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